

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 31, 2003, 13:28:52 ; Search time 41 seconds  
(without alignments)  
1233.774 Million cell updates/sec

Title: US-10-082-894-2

Perfect score: 2786

Sequence: 1 MDYQNVQKVCVLWIDGWS.....LMGLPVPEMDGVPLLEQRG 536

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_76.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID    | Description        |
|------------|--------|-------------|--------|----------|--------------------|
| 1          | 1900   | 68.2        | 539    | 2 T32749 | hypothetical prote |
| 2          | 1143.5 | 41.0        | 510    | 2 A11750 | phosphoglycerate m |
| 3          | 1141.5 | 41.0        | 510    | 2 AH1381 | phosphoglycerate m |
| 4          | 1127   | 40.5        | 511    | 2 T46865 | phosphoglycerate m |
| 5          | 1120   | 40.2        | 510    | 2 E84094 | 2,3-bisphosphoglyc |
| 6          | 1118   | 40.1        | 511    | 2 D69675 | phosphoglycerate m |
| 7          | 1088.5 | 39.1        | 515    | 2 G83004 | phosphoglycerate m |
| 8          | 1083.5 | 38.9        | 510    | 2 G82335 | phosphoglycerate m |
| 9          | 1081   | 38.8        | 507    | 2 AF0974 | phosphoglycerate m |
| 10         | 1078   | 38.7        | 533    | 2 AG2328 | 2,3-bisphosphoglyc |
| 11         | 1073.5 | 38.5        | 515    | 2 AH0008 | phosphoglycerate m |
| 12         | 1065   | 38.2        | 510    | 2 F96987 | 2,3-bisphosphoglyc |
| 13         | 1063   | 38.2        | 514    | 2 S47833 | probable phosphogl |
| 14         | 1059   | 38.0        | 514    | 2 B91190 | hypothetical prote |
| 15         | 1059   | 38.0        | 514    | 2 C86037 | hypothetical prote |
| 16         | 1055   | 37.9        | 510    | 2 A56142 | phosphoglycerate m |
| 17         | 1023   | 36.7        | 508    | 2 S73540 | phosphoglycerate m |
| 18         | 1023   | 36.7        | 532    | 2 S76482 | probable phosphogl |
| 19         | 999.5  | 35.9        | 505    | 2 AD2983 | hypothetical prote |
| 20         | 999.5  | 35.9        | 505    | 2 C98300 | hypothetical prote |
| 21         | 996    | 35.8        | 491    | 2 F64641 | probable phosphogl |
| 22         | 991    | 35.6        | 491    | 2 G71872 | 2,3-bisphosphoglyc |
| 23         | 990.5  | 35.6        | 534    | 2 S73300 | phosphoglycerate m |
| 24         | 975    | 35.0        | 505    | 2 H89850 | hypothetical prote |
| 25         | 967.5  | 34.7        | 508    | 2 G84339 | phosphoglycerate m |
| 26         | 961.5  | 34.5        | 510    | 2 S42705 | probable phosphogl |
| 27         | 955.5  | 34.3        | 507    | 2 E64247 | phosphoglycerate m |
| 28         | 894.5  | 32.1        | 492    | 2 H81387 | phosphoglycerate m |
| 29         | 844.5  | 30.3        | 505    | 2 C90569 | hypothetical prote |

ALIGNMENTS

RESULT 1

T32749

hypothetical protein F57B10.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 21-Jan-2000

C;Accession: T32749

R;Greco, T.; Elliott, G.; Keppler, D.

submitted to the EMBL Data Library, December 1997

A;Description: The sequence of C. elegans cosmid F57B10.

A;Reference number: Z21219

A;Accession: T32749

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-539 <GRE>

A;Cross-references: EMBL:AF039713; PIDN:AAE96720.1; GSPDB:GN00019; CESP:F57B10.3

A;Experimental source: strain Bristol N2; clone F57B10

C;Genetics:

A;Gene: CESP:F57B10.3

A;Map position: 1

A;Introns: 18/1; 64/1; 115/3; 151/1; 200/2; 242/3; 387/3; 503/3

C;Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent

Query Match 68.2%; Score 1900; DB 2; Length 539;

Best Local Similarity 66.7%; Pred. No. 6.6e-145;

Matches 352; Conservative 76; Mismatches 86; Indels 14; Gaps 5;

|    |     |   |     |
|----|-----|---|-----|
| Qy | 1   | MDKYQNVQKVCVLWIDGWSDEQHGNAIAKAKTPIMDKLCSGNWOKLEAHGLHVLGPE     | 60  |
| Db | 21  | MANNSSVANKVCVLWIDGWSDEDPYGNAILNAQTVMYDKLCSGNWQIAEAGHLVGLPE    | 80  |
| Qy | 61  | GLMGNSEVGHNLICAGRVIVQDIVRINLAVQNEFVNQIVASAEAKKSGRLHLGL        | 120 |
| Db | 81  | GLMGNSEVGHNLICAGRVIVQDIVRINLAVKNNFVNESLVDACRKNNGRLHLGL        | 140 |
| Qy | 121 | VSDGCVSHSHDHPALIRAFKQLQKPVVFIFHFDAGDRDTSPTSGAGVLEQLQFIASEK-   | 179 |
| Db | 141 | VSDGCVSHSHDHPALIRAFKQLQKPVVFIFHFDAGDRDTSPTSGAGVLEQLQFIASEK-   | 198 |
| Qy | 180 | --YGEIATITGRYYAMDRLKRWIRIKMAYEIVGIGGIGOKATVDKAVDVVRERYAQSETE  | 237 |
| Db | 199 | TYGKGLATVGRYYAMDRLKRWIRIKMAYEIVGIGGIGOKATVDKAVDVVRERYAQSETE   | 258 |
| Qy | 238 | FLKPIFV-SDDGRVKKDDDTLFFNVRADRMQICEGLGLERYKDLNSVVPKNIQSGM      | 296 |
| Db | 259 | FLKPIIILQEGKRVONDDTIFFDYRADRMREISAMGMMDRYKDCNSKLAHPNSLVQVGM   | 318 |
| Qy | 297 | TOYNKEFPFSLFPVTHNVLAESQGVTFQHCATEKYKYPHVTFFNGREVFQODE         | 356 |
| Db | 319 | TOYKAEFPFSLFPVTHNVLAESQGVTFQHCATEKYKYPHVTFFNGREVFQODE         | 378 |
| Qy | 357 | ERCMPVPKPEVATYDLKPEMNAAGVAEKWYEQIESGRHPLVMCMFPAPDMVGHGTGKFPFA | 416 |

Db 379 ERCLVSPK-VATYDLOPEMSAGVADKMIQLEAGTHPFIOMCFAPPDMVGHGTGYEAA 437  
QY 417 VRACQATDAIGKIFACQTYNVLMVTSDHGNAEKMIAPDGSEHTAHTCNLVPTFCSSK 476  
Db 438 VRACEATDAIGRIEATQKHGYSLVMTADHGNAEKAPDGGKHTAHTCYRVPLTSLRP 497  
QY 477 TFVFKSTPTGDDGKERARALRDVAPTIVQLMGLPVPPEMDGVPPLLEQ 524  
Db 498 GKRFV-----DPADRHPCALCDVAPTIVLAINGLPQPAEMTGVSIQVK 538  
RESULT 2  
AII1750  
phosphoglycerate mutase homolog pgm [imported] - *Listeria innocua* (strain Clip11262)  
C:Species: *Listeria innocua*  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 14-Dec-2001  
C:Accession: AII1750  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker  
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.  
Science 294, 849-852, 2001  
A:Authors: Krefte, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,  
ok C.; Schlueter, T.; Simoes, N.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma  
A:Title: Comparative genomics of *Listeria* species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AII1750  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-510 <GLA>  
A:Cross-references: GB:AL592022; PIDN:CAC97777.1; PID:g16415072; GSPDB:GN00178  
A:Experimental source: strain Clip11262  
C:Genetics:  
A:Gene: pgm  
C:Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent  
Query Match 41.0%; Score 1143.5; DB 2; Length 510;  
Best Local Similarity 44.2%; Pred. No. 5.3e-84;  
Matches 231; Conservative 91; Mismatches 174; Indels 27; Gaps 7;  
QY 11 VCLWIDGWSLDEQHGNAIAKATPIMDKLCSGNWQ-----KLEAHGLHVLGPEGLMGN 65  
Db 6 VAIILIDGFGKRAETVGNVAQANKPNFDY----WAFPHGELKAAGLDVGLPEQOMGN 61  
QY 66 SEVGHNLNIGAGRIYQDIVIRINLAVORNEFTVNPQIVASAEKKGSRHLHLGLVSDGG 125  
Db 62 SEVGHNLNIGAGRIYQSLTRIDKAIEGEGFQENKALNNAFTHTKENNSDLHLFLGLSDGG 121  
QY 126 VSHIDHLPALRAFQLOVPKVFTHFFADGRDTSPTSCAGYLEQLLOFIASEKYGELAT 185  
Db 122 VSHINHLVALLTAKDKGKVNYYTHAFLDGRDVAPOSSLEYLETLEKAIKSLNLYGAIAT 181  
QY 186 ITGRYVAMDRDKRWERIKMAYEAIYGGIGOKATVDKAVDVVRERYAQSTDEFKLPVFS 245  
Db 182 VSGRFYAMDRDKRWERIKMAYEAIYGGIGOKATVDKAVDVVRERYAQSTDEFKLPVFS 239  
QY 246 DGR-----VKDDTLFFNYRADRMQICEGLGLERYKDLNLSVPHPKNIQISGMTQYNK 301  
Db 240 KDGKPVATVTKNDVAIVFFNFRPDRAIQLSNAFTDKEDWDFRGADHPKNIKFTVMTLYNP 299  
QY 302 EFPFSLFPVTHVNLAEWLASQGVTPQFHCATEKYPHVTFFNFGREVQFQDERCMV 361  
Db 300 STDAEVAEPTEMKNVIGEVLSQSLRIATEKYPHVTFFNFGREVQFQDERCMV 359  
QY 362 PSPKEVATYDLKPEMNAAGVAKMVEQIESGRHPLVMCFNFPDMVGHGKPEPAVKACQ 421  
Db 360 NSPK-VETVYDLKPEMSAYEVTALVEDIKNDKHAIIILNFANPDVGVHSGMLEPTIKAE 418  
QY 422 ATDEAIGKIFACQTYNVLMVTSDHGNAEKMIAPDGSEHTAHTCNLVPTFCSSKTFVK 481  
Db 419 AVDENLGRVVDLILEKGGSAIIFADHGNSETMSTPEGKPHATHTVPVPIVTKK----- 473  
QY 482 STPTGDDGKERARALRDVAPTIVQLMGLPVPPEMDGVPPLLEQ 524

Db 474 -----GVTLREGGR-LADVAPTMLDILLGVKKPAEMTGESLIQK 510  
RESULT 3  
AII1381  
phosphoglycerate mutase homolog pgm [imported] - *Listeria monocytogenes* (strain EGD 3  
C:Species: *Listeria monocytogenes*  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 14-Dec-2001  
C:Accession: AII1381  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker  
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.  
Science 294, 849-852, 2001  
A:Authors: Krefte, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma  
ok C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,  
A:Title: Comparative genomics of *Listeria* species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AII1381  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-510 <GLA>  
A:Cross-references: GB:NC\_003210; PIDN:CAD00534.1; PID:g16411944; GSPDB:GN00177  
A:Experimental source: strain EGD-3  
C:Genetics:  
A:Gene: pgm  
C:Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent  
Query Match 41.0%; Score 1141.5; DB 2; Length 510;  
Best Local Similarity 44.0%; Pred. No. 7.7e-84;  
Matches 230; Conservative 92; Mismatches 174; Indels 27; Gaps 7;  
QY 11 VCLWIDGWSLDEQHGNAIAKATPIMDKLCSGNWQ-----KLEAHGLHVLGPEGLMGN 65  
Db 6 VAIILIDGFGKRAETVGNVAQANKPNFDY----WAFPHGELKAAGLDVGLPEQOMGN 61  
QY 66 SEVGHNLNIGAGRIYQDIVIRINLAVORNEFTVNPQIVASAEKKGSRHLHLGLVSDGG 125  
Db 62 SEVGHNLNIGAGRIYQSLTRIDKAIEGEGFQENKALNNAFTHTKENNSDLHLFLGLSDGG 121  
QY 126 VSHIDHLPALRAFQLOVPKVFTHFFADGRDTSPTSCAGYLEQLLOFIASEKYGELAT 185  
Db 122 VSHINHLVALLTAKDKGKVNYYTHAFLDGRDVAPOSSLEYLETLEKAIKSLNLYGAIAT 181  
QY 186 ITGRYVAMDRDKRWERIKMAYEAIYGGIGOKATVDKAVDVVRERYAQSTDEFKLPVFS 245  
Db 182 VSGRFYAMDRDKRWERIKMAYEAIYGGIGOKATVDKAVDVVRERYAQSTDEFKLPVFS 239  
QY 246 DGR-----VKDDTLFFNYRADRMQICEGLGLERYKDLNLSVPHPKNIQISGMTQYNK 301  
Db 240 KDGKPVATVTKNDVAIVFFNFRPDRAIQLSNAFTDKEDWDFRGADHPKNIKFTVMTLYNP 299  
QY 302 EFPFSLFPVTHVNLAEWLASQGVTPQFHCATEKYPHVTFFNFGREVQFQDERCMV 361  
Db 300 STDAEVAEPTEMKNVIGEVLSQSLRIATEKYPHVTFFNFGREVQFQDERCMV 359  
QY 362 PSPKEVATYDLKPEMNAAGVAKMVEQIESGRHPLVMCFNFPDMVGHGKPEPAVKACQ 421  
Db 360 NSPK-VETVYDLKPEMSAYEVTALVEDIKNDKHAIIILNFANPDVGVHSGMLEPTIKAE 418  
QY 422 ATDEAIGKIFACQTYNVLMVTSDHGNAEKMIAPDGSEHTAHTCNLVPTFCSSKTFVK 481  
Db 419 AVDENLGRVVDLILEKGGSAIIFADHGNSETMSTPEGKPHATHTVPVPIVTKK----- 473  
QY 482 STPTGDDGKERARALRDVAPTIVQLMGLPVPPEMDGVPPLLEQ 524  
Db 474 -----GVTLREGGR-LADVAPTMLDILLGVKKPAEMTGESLIQK 510  
RESULT 4  
T46865  
phosphoglycerate mutase (EC 5.4.2.1), 2,3-diphosphoglycerate-independent [validate=]  
C:Species: *Bacillus stearothermophilus*  
C:Date: 17-Mar-2000 #sequence\_revision 17-Mar-2000 #text\_change 18-Aug-2000



A:Cross-references: GB:299121; GB:AL009126; NID:g2635827; PIDN:CAB15396.1; PID:g2635904  
A:Experimental source: strain 168  
R:Leiva-Vazquez, M.A.; Setlow, P.  
J. Bacteriol. 176, 3903-3910, 1994  
A:Title: Cloning and nucleotide sequences of the genes encoding triose phosphate isomerase  
A:Reference number: 140022; MUID:94292408; PMID:80211172  
A:Accession: 140024  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-232, 'C', 234-431, 'MV', 434-444, 'D', 446-511 <RES>  
A:Cross-references: GB:L29475; NID:g460256; PIDN:AA21680.1; PID:g460258  
C:Genetics:  
A:Gene: pgm  
C:Function:  
A:Description: EC 5.4.2.1 [validated, MUID:94292408]  
A:Note: 2,3-bisphosphoglycerate-independent but M2+2-dependent enzyme [validated, MUID:94292408]  
C:Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent  
C:Keywords: intramolecular transferase; isomerase

Query Match 40.1%; Score 1118; DB 2; Length 511;  
Best Local Similarity 42.7%; Pred. No. 6.1e-82;  
Matches 225; Conservative 99; Mismatches 175; Indels 28; Gaps 6;

QY 8 QQKVLVVDGSLSDQHGNAIAKAKTPIMDKLCSGNW-----QKLEAHLHVLPEGL 62  
Db 3 KKPAAIILDFGLRNETVGNVALAKKPNFDRY---WNOYPHOTLTASGEAVLPEQ 58  
QY 63 MGNSEVGHNLGAGRIYQIDVRINLAVORNEFTNPQIVASAEAKKGGRLHLLGLVS 122  
Db 59 MGNSEVGHNLGAGRIYQSLTRVNVAIREFEERQTFDLAISNAKENKALHLLGLLS 118  
QY 123 DGVVSHIDLHLAFKALQKQVPIHFADGRDTSPTSGAGYLEQLQFIASEKYGELATITGRY 182  
Db 119 DGVVSHINHLFALLKAKKGLTKVYIHGFLDGRDVGTPQAKTYINQLNDQIKELGVGE 178  
QY 183 LATITGRYAMDRKWERIKMAYEALVGGIGQKATVDKAVDVVRYRYAQSEDEFKPI 242  
Db 179 IASIGRYSMDRKWRDVEKAYRAMAYGEG--PSYRSALVDVDSYANGIYDEFVIPS 236  
QY 243 VFSDD-----GRVKDDDTLFFNYRADRMQICECLGLERYKOLNSVPHPKNIQISGMT 297  
Db 237 VITKENGEPVAKIQDGSVIFYNFRPDRAIQISNTTNKDFRDFRGENYPKNLYFVCLT 296  
QY 298 QYNKEFPFSLFPVTHNVLAELWLASQGVTPHCAETEKYPHVTFFNGRGVQFQDEE 357  
Db 297 HFSETVDGYVAFKPINLNTVGEVLVSHQGLKQLRIAEATEKYPHVTFFMSSGGEAEFPGE 356  
QY 358 RCMVSPKEVATYDLAPENNAAGVAEKVQIESGRHPLVMCFAPPDVMVGHGKFERAV 417  
Db 357 RIILNSPK-VATYDLAPENSAEYVKDALKEIEADKHAILNFANPDVMVGHSGWVEPTI 415  
QY 418 KACQATDEAIGKIFEACQYNNVLMVTSDHGNAEKMAPDGSSEHTAHTCNLPFTCSSKT 477  
Db 416 KATEAVDECLGEVVDAILAKGHAITADHGNADILITESGEPTAHTNPVPVITKEG 475  
QY 478 FVFKSTPTPGDDGKERARALRDVAPTVLQMLGPPVPEMDGVPLLEQ 524  
Db 476 ITLR-----EGGILGDLAPTLLDLGVEKPEKMTGTSLOK 511

RESULT 7  
G83004  
Phosphoglycerate mutase PA5131 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: G83004  
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; Br  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
N.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: G83004

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-515 <STO>  
A:Cross-references: GB:AE004926; GB:AE004091; NID:g9951424; PIDN:AA08516.1; GSPDB:N  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: pgm; PA5131  
C:Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent

Query Match 39.1%; Score 1088.5; DB 2; Length 515;  
Best Local Similarity 45.0%; Pred. No. 1.5e-79;  
Matches 232; Conservative 78; Mismatches 180; Indels 25; Gaps 9;

QY 13 LVVDGWSLSDQHGNAIAKAKTPIMDKLCSGNWQKL-EAHLGHLHVLPEGLMGNSEVGH 71  
Db 10 LIILDFGHSFSDYNAIYAAKPVWDRLLATQPHGLISGSGMDVGLPQMGSEVGHM 69  
QY 72 NTGAGRIYQIDVRINLAVORNEFTNPQIVASAEAKKGGRLHLLGLVSDGVVSHID 131  
Db 70 NLGAGRIYQIDFTRVTKAIRDGEFFENVIAGAVDKAADAHVHILGLLSPGVVSHED 129  
QY 132 HLFALIRAFKQKQVPIHFADGRDTSPTSGAGYLEQLQFIASEKYGELATITGRY 191  
Db 130 HLVAQMAARAGAGKIYILHAFLDGRDTPPKSAQPSLERLDATFAGLGKRIASIIIGRYF 189  
QY 192 ANDRDKRWIRIKMAYEALVGGIGQKATVDKAVDVVRYRYAQSEDEFKPIVFSDDG--- 248  
Db 190 ANDRDNRWDRVQAAYELIVDGKAE-FTADSSVAALAEAYARGESDEFVAKATAVVPAGAE 248  
QY 249 -RVKDDDTLFFNYRADRMQICECLGLERYKOLNSVPHPKNIQISG---MTQYNKEPP 304  
Db 249 VRVEDGDAVIFNFRADRAELSRFAVEPAFNEF----PRERAPQALAGEVMTLQYAASTP 304  
QY 305 FFSRLPPVTHNVLAELWLASQGVTPHCAETEKYPHVTFFNGRGVQFQDERCMVSP 364  
Db 305 ACAPFPPELTNVLGELAKHKTQRIAEATEKYPHVTFFSGRREPTGEGERIILPSP 364  
QY 365 KEVATYDLAPENNAAGVAEKVQIESGRHPLVMCFAPPDVMVGHGKFERAVKACQATD 424  
Db 365 K-VATYDLQPEMSAPEVTORIVEAIEQRYDVIVVNYANGDMVGHGTFEAAVKAVECLD 423  
QY 425 EAIGKIFEACQYNNVLMVTSDHGNAEKM-IAPDGESEHTAHTCNLPFTCSSKTFFVKST 483  
Db 424 TCMGRIVEALDKVGGELITADHGNVEQMEDESTGQATHTAHTCEPVPP-----VYVGKRR 478  
QY 484 PPTGDDGKERARALRDVAPTVLQMLGPPVPEMDG 518  
Db 479 LSIREGG-----VLADVAPTMLTLMGLEQPAEMTG 508

RESULT 8  
G82335  
phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent VC0336 [imported] - V  
C:Species: Vibrio cholerae  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
C:Accession: G82335  
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, J  
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellens  
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A:Reference number: A82035; MUID:20406833; PMID:10952301  
A:Accession: G82335  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-510 <HEI>  
A:Cross-references: GB:AE004122; GB:AE003852; NID:g9654745; PIDN:AAF93509.1; GSPDB:3N  
A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
C:Genetics:  
A:Gene: VC0336  
A:Map position: 1  
C:Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent



Db 185 VSGRYVAMDRDRWRVQRDAYVMTQGVGDGR---KAVDVLQASVAGVNDFFIVPVR 241  
Qy 245 SDDGRVKDDTLFFNYRADMRQIC-----ECLGLERYKDLNSSLVPHPKNIQISQWTQ 298  
Db 242 A-PGTVPGDGVIFNFRPDRSRLQTAQAFVSPEFTGARQQ-----IKPLSFTFTQ 292  
Qy 299 YNKEFPFPPSLFPVTHNVLAELASQVYQFHCAETEKYPHVTFFNGGREGVQFODEER 358  
Db 293 YSDLSVSAFEPQNLNLTILGIEVIANQGLNFRTAETEKYAHVTYFFNGGLEPFAGEDR 352  
Qy 359 CMVPSKEVATYDLKPEMNAAGVAEKVQIESGRHPLVMCNFAPDMVGHGKFPAPV 418  
Db 353 ELVSSPM-VATYDKAPASATVDTAIAIQIYSLVINYANPDVGHGTOIEPTIK 411  
Qy 419 ACQATDEAIGKIFACQTYNVLMVTSDHGNAEKMIAPDGESEHTAHTCNLPVPTCSKTF 478  
Db 412 AIVTDRCLGRLEGVSKAGGTIIITADHGNAEVMDLDEAGNSWTAHTNPVPLLYVEGEK 471  
Qy 479 V----FKSTPTGDDGKERARALRDVAPTVLQMLGLPVPPMDGVPLLE 523  
Db 472 VKIPGYGTNVELRSDGK-----LADIAPTILDLQLPQPPMTGRSLIQ 515

RESULT 11  
AH0008  
phosphoglycerate mutase (EC 5.4.2.1) [imported] - Yersinia pestis (strain CO92)  
C:Species: Yersinia pestis  
C>Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 27-Nov-2001  
C:Accession: AH0008  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Li, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AH0008  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-515 <R>  
A:Cross-references: GB:AL590842; PIDN:CAC88930.1; PID:g15978177; GSPDB:GN00175  
C:Genetics:  
A:Gene: YPO0064  
C:Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent  
C:Keywords: intramolecular transferase; isomerase

Query Match 38.5%; Score 1073.5; DB 2; Length 515;  
Best Local Similarity 41.7%; Pred. No. 2.4e-78;  
Matches 222; Conservative 95; Mismatches 176; Indels 39; Gaps 10;

Qy 6 NVQOKVCLVVDGWSLSDQHGNAIAKATPIMDKLCSGNWQK-----LEAGLHVGLPE 60  
Db 3 STKKPLVLTLDGYGHREEQDNAILNAKTPVMDVL----WQOQPHTLIAASGLDYLDP 58  
Qy 61 GLMGNSEVGHNLGACRVYQDITVRINLAVORNEFTNPQIVASAEKKGSRLLHGL 120  
Db 59 GQMGNEVGHNLGACRVYQDITRDLKKEIGEDFTNTPLTAADVNAVKTCKAVHIMGL 118  
Qy 121 VSDGVVSHIDLHALIRAFKQLQVQVFIHFFADGRDTSPTSGAGYLEQLQLQFTASEKY 180  
Db 119 LSAGGVSHSHEDHIMAVELAAKRGATAIYHAFLDGRDTPPRSSESLRAKFAELGN 178  
Qy 181 GELATITGRYAMDRKRERIKMAYEATVGGIGQKATVDKADVVRERYAQSEDTDFLK 240  
Db 179 GRIASIGRYAMDRNRVQLAYDLTQARKE-FTADNAVAGLQAAYARGENDEFYK 237  
Qy 241 PIVF-----SDGGRVKDDTLFFNYRADMRQI-----CECGLERYKDLNSSLVPHPKN 290  
Db 238 PTVIQATGADAMNEDGLIFNFRADRARQITRTFVNAEDFGKRVKWNFG----- 291  
Qy 291 IOISGMYNQNEFPFSLFPVTHNVLAELASQVQFHCAETEKYPHVTFFNGGREG 350  
Db 292 -DFIMLEYAADIKVCACVAPPASLTNTFCEMLMKHDKTQLRISETEKYAHVTFFNGGVE 350

Qy 351 VQFQDEERCWVSPKEVATYDLKPEMNAAGVAEKVQIESGRHPLVMCNFAPDMVGH 410  
Db 351 EPFGEDRILINSPK-VATYDLQPESSAELTEKLVSAIGSKYDVLICNYPNGDMVGH 409  
Qy 411 GXFEPVAKACQATDEAIGKIFACQTYNVLMVTSDHGNAEKMIAP-DGSEHTAHTCNLV 469  
Db 410 GYDAAVKAVETLQNCIEQVAAVKAADGQLLTADHGNAEQMRDQATGOAHTAHTSLPV 469  
Qy 470 PFTCSKSTVFVKSTPTPTGDDGKERARALRDVAPTVLQMLGLPVPPMDGVPL 521  
Db 470 PL-----IYGNKAVKAVEGK-----LSDIAPTMLSLMEMEIPQEMTKPL 511

RESULT 12  
F96987  
2,3-bisphosphoglycerate-independent phosphoglycerate mutase gene [imported] - Clostridium acetobutylicum  
C:Species: Clostridium acetobutylicum  
C>Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 30-Sep-2001  
C:Accession: F96987  
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: F96987  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-510 <R>  
A:Cross-references: GB:AE001437; PIDN:AAK78689.1; PID:g15023592; GSPDB:GN00168  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC0712  
C:Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent

Query Match 38.2%; Score 1065; DB 2; Length 510;  
Best Local Similarity 42.9%; Pred. No. 1.1e-77;  
Matches 225; Conservative 99; Mismatches 176; Indels 24; Gaps 10;

Qy 8 QOKVCLVVDGWSLSDQHGNAIAKATPIMDKLCSGNW--OKLEAHGLHVLGPEGLMN 65  
Db 3 KKPVMILMDGFGISDKVDGNVAKAASKPNFDKFN-NYPHTHLGASGLSVGLPDQMG 61  
Qy 66 SEVGHNLGACRVYQDITVRINLAVORNEFTNPQIVASAEKKGSRLLHGLVSDGG 125  
Db 62 SEVGHNLGACRVYQSLTKITKATDGDGFFKNAALNKAVNVLENDSTLHLMGLSPG 121  
Qy 126 VHSHTDHLFALLRAFKQLQVQVFIHFFADGRDTSPTSGAGYLEQLQLQFTASEKYELAT 185  
Db 122 VHSHTNHLKGLQLAKKNVKKVFFHAFLDGRDVPSSAKFEIKDIEDYVNEIGLGEIAT 181  
Qy 186 ITGRYAMDRKRERIKMAYEATVGGIGQKATVDKADVVRERYAQSEDTDFLKPIVES 245  
Db 182 VSGRYAMDRNREREELAYNAMVLGGEA--ESAIAKADVASHDNKTDDEFVLPTIV 239  
Qy 246 DDGR-----VKDDTLFFNYRADMRQICEGLERYKDLNSSLVPHPKNIQISGMYQNK 301  
Db 240 KECKPVATIKDSDVIFNFRDRAQITRAAEAFDGFKRD---RLNIEFVMTVEYDA 296  
Qy 302 EPPFSL-FPPVTHNVLAELASQVQFHCAETEKYPHVTFFNGGREGVQFODERCM 360  
Db 297 SFKGVDAFAGPENITNLTGEEVSNKGLNQLRTAETEKYAHVTFFNGGVEEENKNDRL 356  
Qy 361 VSPKEVATYDLKPEMNAAGVAEKVQIESGRHPLVMCNFAPDMVGHGKFPAPVAKAC 420  
Db 357 ISSPK-VATYDLKPEMSAVETDELKRLDDEKDYMWILNANPDVGHGTOIEAARAKAV 415  
Qy 421 QATDEAIGKIFACQTYNVLMVTSDHGNAEKMI-APDGESEHTAHTCNLPVPTCSKTFV 479  
Db 416 ETVDCECLGKIVDKLGDGVFIADHGNSEQIMIDYSGNKPMTAHTVNPVPF-----YVV 470  
Qy 480 FKSTPTGDDGKERARALRDVAPTVLQMLGLPVPPMDGVPLLE 523  
Db 471 SNHT-----EAKNLGCVLADIAPTMLQEMGLEKPEMTGKSLFE 510



